

### **INPUT SET: S11218.raw**

**This Raw Listing contains the General Information Section and those Sequences containing ERRORS.**

## **ERRORED SEQUENCES FOLLOW:**

INPUT SET: S11218.raw

61 (2) INFORMATION FOR SEQ ID NO:2:  
62  
63 (i) SEQUENCE CHARACTERISTICS:  
64 (A) LENGTH: 17 amino acids  
65 (B) TYPE: amino acid  
66 (C) STRANDEDNESS: single  
67 (D) TOPOLOGY: linear  
68  
69 (ii) MOLECULE TYPE: DNA (genomic)  
70  
71 (iii) HYPOTHETICAL: NO  
72  
73 (iv) ANTI-SENSE: YES  
74  
75 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
76  
77 GAGAGGAAAAA  
78  
79  
80

Discrepancy  
Please review  
carefully &  
ed! +  
accordingly.

10

81 (2) INFORMATION FOR SEQ ID NO:3:  
82  
83 (i) SEQUENCE CHARACTERISTICS:  
84 (A) LENGTH: 10 base pairs  
85 (B) TYPE: PNA  
86 (C) STRANDEDNESS: single  
87 (D) TOPOLOGY: linear  
88  
89 (ii) MOLECULE TYPE: PNA ← ok, here  
90  
91 (iii) HYPOTHETICAL: NO  
92  
93 (iv) ANTI-SENSE: YES  
94  
95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
96  
97 TTTTCCTCTC 10  
98  
99  
100  
101

102 (2) INFORMATION FOR SEQ ID NO:4:  
103  
104 (i) SEQUENCE CHARACTERISTICS:  
105 (A) LENGTH: 10 base pairs  
106 (B) TYPE: PNA  
107 (C) STRANDEDNESS: single  
108 (D) TOPOLOGY: linear  
109  
110 (ii) MOLECULE TYPE: PNA  
111

nucleic acid

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/612,661DATE: 06/22/96  
TIME: 13:24:35

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112 (iii) HYPOTHETICAL: NO  
113  
114 (iv) ANTI-SENSE: YES  
115  
116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
117  
118  
--> 119 TTTTCNTCTC 10  
120  
121  
122

---

123 (2) INFORMATION FOR SEQ ID NO:5:  
124  
125 (i) SEQUENCE CHARACTERISTICS:  
--> 126 (A) LENGTH: 10 base pairs  
--> 127 (B) TYPE: PNA  
128 (C) STRANDEDNESS: single  
129 (D) TOPOLOGY: linear  
130  
131 (ii) MOLECULE TYPE: PNA  
132  
133 (iii) HYPOTHETICAL: NO  
134  
135 (iv) ANTI-SENSE: YES  
136  
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
138  
139  
--> 140 TTTTCNTNTC 10  
141  
142  
143

---

144 (2) INFORMATION FOR SEQ ID NO:6:  
145  
146 (i) SEQUENCE CHARACTERISTICS:  
--> 147 (A) LENGTH: 10 base pairs  
--> 148 (B) TYPE: PNA  
149 (C) STRANDEDNESS: single  
150 (D) TOPOLOGY: linear  
151  
152 (ii) MOLECULE TYPE: PNA  
153  
154 (iii) HYPOTHETICAL: NO  
155  
156 (iv) ANTI-SENSE: YES  
157  
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
159  
--> 160 TTTTNNTCTC 10  
161  
162

RAW SEQUENCE LISTING  
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163

205 (2) INFORMATION FOR SEQ ID NO:9:

206

207 (i) SEQUENCE CHARACTERISTICS:

208 (A) LENGTH: 10 base pairs

--&gt; 209 (B) TYPE: PNA

210 (C) STRANDEDNESS: single

211 (D) TOPOLOGY: linear

212

213 (ii) MOLECULE TYPE: PNA

214

215 (iii) HYPOTHETICAL: NO

216

217 (iv) ANTI-SENSE: YES

218

219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

220

221 AGTCACCTAC

10

222

223

224

225 (2) INFORMATION FOR SEQ ID NO:10:

226

227 (i) SEQUENCE CHARACTERISTICS:

228 (A) LENGTH: 10 base pairs

--&gt; 229 (B) TYPE: PNA

230 (C) STRANDEDNESS: single

231 (D) TOPOLOGY: linear

232

233 (ii) MOLECULE TYPE: PNA

234

235 (iii) HYPOTHETICAL: NO

236

237 (iv) ANTI-SENSE: YES

238

239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

240

241

242 AGTCANCTAC

10

243

244

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/08/612,661

INPUT SET: S11218.raw

Line	Error	Original Text	
64	Entered (17) and Calc. Seq. Length (0) differ	(A) LENGTH: 17 amino acids	
77	Wrong Amino Acid Designator	GAGAGGAAAA	10
84	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
85	Wrong or Missing Sequence Type	(B) TYPE: PNA	
97	Wrong Amino Acid Designator	TTTTCCTCTC	10
105	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
106	Wrong or Missing Sequence Type	(B) TYPE: PNA	
119	Wrong Amino Acid Designator	TTTTCNTCTC	10
126	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
127	Wrong or Missing Sequence Type	(B) TYPE: PNA	
140	Wrong Amino Acid Designator	TTTTCNTNTC	10
147	Entered (10) and Calc. Seq. Length (0) differ	(A) LENGTH: 10 base pairs	
148	Wrong or Missing Sequence Type	(B) TYPE: PNA	
160	Wrong Amino Acid Designator	TTTTNNNTCTC	10
209	Wrong or Missing Sequence Type	(B) TYPE: PNA	
229	Wrong or Missing Sequence Type	(B) TYPE: PNA	

08/6/2661

## Notice of Availability

### Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the *PTO Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the *PTO Official Gazette*.

The software can be accessed/requested in the following locations:

- 1) Dial-up access to the Patent and Trademark Office Bulletin Board System.  
Phone number: 703-305-8950  
Cost: Free-of-charge
- 2) Dial-up access through the Internet. FTP site: [ftp.uspto.gov](ftp://ftp.uspto.gov)  
Login as "anonymous". Software is in directory /pub/checker  
Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-306-2600.  
Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-4212.